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SMART MODE:

NORMAL GENOMIC

Schultz et al. (1998) *Proc. Natl. Acad. Sci. USA* **95**, 5857-5864
Letunic et al. (2008) *Nucleic Acids Res* , doi:10.1093/nar/gkn808

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HTH_LUXR

HTH
LUXR

helix_turn_helix, Lux Regulon

SMART accession number:	SM00421
Description:	lux regulon (activates the bioluminescence operon

This domain is a DNA-binding, helix-turn-helix (HTH) domain of about 65 amino acids, present in transcription regulators of the LuxR/FixJ family of response regulators. The domain is named after Vibrio fischeri luxR, a transcriptional activator for quorum-sensing control of luminescence. LuxR-type HTH domain proteins occur in a variety of organisms. The DNA-binding HTH domain is usually located in the C-terminal region; the N-terminal region often containing an autoinducer-binding domain or a response regulatory domain. Most luxR-type regulators act as transcription activators, but some can be repressors or have a dual role for different sites. LuxR-type HTH regulators control a wide variety of activities in various biological processes.

The luxR-type, DNA-binding HTH domain forms a four-helical bundle structure. The HTH motif comprises the second and third helices, known as the scaffold and recognition helix, respectively. The HTH binds DNA in the major groove, where the N-terminal part of the recognition helix makes most of the DNA contacts. The fourth helix is involved in dimerisation of gerE and traR. Signalling events by one of the four activation mechanisms described below lead to multimerisation of the regulator. The

regulators bind DNA as multimers (PUBMED:11243786), (PUBMED:12740396), (PUBMED:12087407).

LuxR-type HTH proteins can be activated by one of four different mechanisms:

1) Regulators which belong to a two-component sensory transduction system where the protein is activated by its phosphorylation, generally on an aspartate residue, by a transmembrane kinase (PUBMED:12352954), (PUBMED:12162958). Some proteins that belong to this category are:

- Rhizobiaceae fixJ (global regulator inducing expression of nitrogen-fixation genes in microaerobiosis)
- Escherichia coli and Salmonella typhimurium uhpA (activates hexose phosphate transport gene uhpT)
- E. coli narL and narP (activate nitrate reductase operon)
- Enterobacteria rcsB (regulation of exopolysaccharide biosynthesis in enteric and plant pathogenesis)
- Bordetella pertussis bvgA (virulence factor)
- Bacillus subtilis coma (involved in expression of late-expressing competence genes)

Interpro abstract (IPR000792):

2) Regulators which are activated, or in very rare cases repressed, when bound to N-acyl homoserine lactones, which are used as quorum sensing molecules in a variety of Gram-negative bacteria (PUBMED:15255890):

- V. fischeri luxR (activates bioluminescence operon)
- Agrobacterium tumefaciens traR (regulation of Ti plasmid transfer)
- Erwinia carotovora carR (control of carbapenem antibiotics biosynthesis)
- E. carotovora expR (virulence factor for soft rot disease; activates plant tissue macerating enzyme genes)
- Pseudomonas aeruginosa lasR (activates elastase gene lasB)
- Erwinia chrysanthemi echR and Erwinia stewartii esaR
- Pseudomonas chlororaphis phzR (positive regulator of phenazine antibiotic production)
- Pseudomonas aeruginosa rhlR (activates rhlAB operon and lasB gene)

3) Autonomous effector domain regulators, without a regulatory domain, represented by gerE (PUBMED:11243786).

- B. subtilis gerE (transcription activator and repressor for the regulation of spore formation)

4) Multiple ligand-binding regulators, exemplified by malT (PUBMED:11931562).

- E. coli malT (activates maltose operon; MalT binds ATP and maltotriose)

GO process: regulation of transcription, DNA-dependent (GO:0006355)

GO component: intracellular (GO:0005622)

GO function: transcription factor activity (GO:0003700), sequence-specific DNA binding (GO:0043565)

Family alignment: View [Alignment consensus sequence] or [Family alignment in] [CHROMA format ▼]

There are 6090 HTH_LUXR domains in 6082 proteins in SMART's nrdb database.

Click on the following links for more information.

- Evolution (species in which this domain is found)
- Literature (relevant references for this domain)
- Metabolism (metabolic pathways involving proteins which contain this domain)
- Structure (3D structures containing this domain)
- Links (links to other resources describing this domain)

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